Amendments to the Claims:

1. (Currently amended) A method of synthesizing a repertoire of oligonucleotide tags, each having a predetermined length in the range of from 18 to 60 nucleotides, the method comprising the steps of:

(a) providing first and second libraries ~~a repertoire~~ of same-length oligonucleotide tag precursors in first and second ~~an amplicon, wherein said amplicon is a~~ cloning vectors,

~~and~~ wherein each oligonucleotide tag precursor consists of ~~one or more~~ two four-nucleotide words, and each word is ~~an oligonucleotide having a length of three to fourteen nucleotides,~~ selected from a minimally cross-hybridizing set of oligonucleotides, such that a duplex consisting of a word of the set and the complement of any other word of the set contains at least two ~~a number of~~ mismatches ~~that is either 1, 2 or 3 less than the length, in nucleotides, of the word~~;

(b) cleaving ~~a first aliquot of the amplicon~~ one such cloning vector, at two cleavage sites, to produce a first opened vector ~~amplicon~~ and a first excised fragment, said first excised fragment containing at most one word from said oligonucleotide tag precursor;

(c) separately cleaving ~~a second aliquot of the amplicon~~ the other such cloning vector, at two cleavage sites, to produce a second opened vector ~~amplicon~~ and a second excised fragment, said second excised fragment containing one or more words from said oligonucleotide tag precursor;

(d) ligating said second excised fragment, containing one or more words, into said first opened vector ~~amplicon~~, thereby elongating said oligonucleotide tag precursors in said first vector ~~aliquot of the amplicon~~;

(e) amplifying the elongated oligonucleotide tag precursors in said first vector ~~aliquot of the amplicon~~; and

(f) repeating steps (b) through (e) until a repertoire of oligonucleotide tags having the predetermined length is formed.

2. (Cancelled)

3. (Currently amended) The method of claim 1, wherein each said step of cleaving includes cleaving said ~~amplicon~~ vector in a region adjacent to said word, using a type IIs restriction endonuclease.

4. (Currently amended) The method of claim 1, wherein each said word ~~has a length in the range of from four to six nucleotides and is constructed from nucleotides selected from A, C, G, and T, or wherein each said word has a length in the range of from four to eight nucleotides and~~ is constructed from three nucleotides selected from A, C, G, and T.

5. (Cancelled)

6. (Currently amended) The method of claim 1, wherein each said step of cleaving includes cleaving said ~~amplicon~~ vector at the upstream and downstream boundaries of a word, using a type IIs restriction endonuclease.

7-14. (Cancelled)

15. (Previously presented) A repertoire of oligonucleotide tags of the form:

$$w_1(N)_{x1}w_2(N)_{x2} \ldots (N)_{xn-1}w_n$$

wherein

each of w_1 through w_n is a word consisting of an oligonucleotide having a length from three to fourteen nucleotides and being selected from a minimally cross hybridizing set, wherein a word of the set and a complement of any other word of the set has a number of mismatches that is either 1, 2 or 3 less than the length of the word, said words being constructed from three of the four natural nucleotides;

N is a nucleotide;

each of x_1 through x_{n-1} is an integer selected from the group consisting of 0, 1, and 2, provided that at least one of x_1 through x_{n-1} is 1 or 2; and

n is an integer in the range of from 4 to 10.

16. (Previously presented) The repertoire of claim 15, wherein said length of each said word is from four to ten nucleotides.

17. (New) The repertoire of claim 15, wherein the length of each said word is four nucleotides.

18. (New) The repertoire of claim 17, wherein each word is selected from a minimally cross-hybridizing set of oligonucleotides such that a duplex consisting of a word of the set and the complement of any other word of the set contains at least three mismatches.

19. (New) The method of claim 1, wherein the first and second cloning vectors are different.

20. (New) The method of claim 1, wherein the first and second cloning vectors are the same.

21. (New) The method of claim 1, wherein each word is selected from a minimally cross-hybridizing set of oligonucleotides such that a duplex consisting of a word of the set and the complement of any other word of the set contains at least three mismatches.